

us-10-038-854-38

GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2004, 21:29:29 ; Search time 2766 Seconds
(without alignments)
5556.365 Million cell updates/sec

Title: US-10-038-854-38

Perfect score: 14495

Sequence: 1 MDVKERRRPPYCSLTKSRRKE.....ELADSANNIQFLRQSEIGRR 2721

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 4176236 seqs, 2824127955 residues

Total number of hits satisfying chosen parameters: 8352472

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10038854_@CGN_1_1_2038_@runat_29122004_112455_10566

us-10-038-854-38
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 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% DB	ID	Description
1	14495	100.0	8645	16	US-10-038-854-37 Sequence 37, Appl
2	14475	99.9	8675	16	US-10-038-854-35 Sequence 35, Appl
3	13944.5	96.2	8473	16	US-10-038-854-39 Sequence 39, Appl
4	13834	95.4	8487	16	US-10-038-854-41 Sequence 41, Appl

5	10403	71.8	8689	9	US-09-808-602-78	Sequence 78, Appl
6	10403	71.8	8689	10	US-09-800-198-66	Sequence 66, Appl
7	10394.5	71.7	8409	9	US-09-808-602-79	Sequence 79, Appl
8	10394.5	71.7	8409	10	US-09-800-198-67	Sequence 67, Appl
9	10394	71.7	8575	16	US-10-072-012-143	Sequence 143, App
10	10393.5	71.7	8797	9	US-09-808-602-74	Sequence 74, Appl
11	10393.5	71.7	8797	9	US-09-808-602-77	Sequence 77, Appl
12	10393.5	71.7	8797	10	US-09-800-198-62	Sequence 62, Appl
13	10393.5	71.7	8797	10	US-09-800-198-65	Sequence 65, Appl
14	10329.5	71.3	8438	16	US-10-042-865-1	Sequence 1, Appli
15	10310.5	71.1	9729	9	US-09-808-602-12	Sequence 12, Appl
16	10310.5	71.1	9729	10	US-09-800-198-12	Sequence 12, Appl
17	10309	71.1	9826	9	US-09-808-602-7	Sequence 7, Appli
18	10309	71.1	9826	10	US-09-800-198-7	Sequence 7, Appli
19	10221	70.5	8354	16	US-10-383-201-43	Sequence 43, Appl
20	10221	70.5	8354	16	US-10-029-020-13	Sequence 13, Appl
21	10078	69.5	9695	15	US-10-144-194A-81	Sequence 81, Appl
22	10078	69.5	9695	18	US-10-491-566-81	Sequence 81, Appl
23	10010	69.1	8355	16	US-10-383-201-55	Sequence 55, Appl
24	9765	67.4	6810	18	US-10-723-860-8301	Sequence 8301, Ap
25	9491	65.5	9058	15	US-10-144-194A-79	Sequence 79, Appl
26	9491	65.5	9058	18	US-10-491-566-79	Sequence 79, Appl
27	9267	63.9	5309	18	US-10-723-860-4493	Sequence 4493, Ap
28	8884	61.3	8297	18	US-10-723-860-4101	Sequence 4101, Ap
29	8884	61.3	12880	15	US-10-295-027-927	Sequence 927, App
30	8463.5	58.4	7781	18	US-10-723-860-2302	Sequence 2302, Ap
31	6894.5	47.6	6771	18	US-10-723-860-6509	Sequence 6509, Ap
32	6702.5	46.2	6560	9	US-09-808-602-76	Sequence 76, Appl
33	6702.5	46.2	6560	10	US-09-800-198-64	Sequence 64, Appl
34	5714	39.4	3614	15	US-10-172-118-1743	Sequence 1743, Ap
35	5714	39.4	3614	16	US-10-342-887-1743	Sequence 1743, Ap
36	4678	32.3	8624	18	US-10-723-860-3169	Sequence 3169, Ap
37	4577.5	31.6	8774	18	US-10-723-860-7176	Sequence 7176, Ap
38	2784	19.2	2496	9	US-09-808-602-75	Sequence 75, Appl
39	2784	19.2	2496	10	US-09-800-198-63	Sequence 63, Appl
40	2316	16.0	1534	18	US-10-128-558-121	Sequence 121, App
41	2263	15.6	3217	14	US-10-198-846-13976	Sequence 13976, A
42	2002	13.8	1399	16	US-10-383-201-49	Sequence 49, Appl
43	2002	13.8	1399	16	US-10-383-201-59	Sequence 59, Appl
44	1954.5	13.5	1371	16	US-10-383-201-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1

US-10-038-854-37

; Sequence 37, Application US/10038854

; Publication No. US20040022781A1

; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Li, Li

; APPLICANT: Wolenc, Adam R

; APPLICANT: Vernet, Corine

; APPLICANT: Eisen, Andrew J

; APPLICANT: Liu, Xiaohong

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Shimkets, Richard A

; APPLICANT: Tchernev, Velizar

; APPLICANT: Spaderna, Steven K

; APPLICANT: Gorman, Linda

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Patturajan, Meera

; APPLICANT: Gusev, Vladimir Y

; APPLICANT: Gangolli, Esha A

; APPLICANT: Guo, Xiaojia S

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Rastelli, Luca

; APPLICANT: Casman, Stacie J

; APPLICANT: Boldog, Ferenc

; APPLICANT: Burgess, Catherine E

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Ellerman, Karen

; APPLICANT: Gunther, Erik

; APPLICANT: Smithson, Glenda

; APPLICANT: Millet, Isabelle

; APPLICANT: MacDougall, John R

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-230

; CURRENT APPLICATION NUMBER: US/10/038,854

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; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 8645
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-038-854-37

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Alignment Scores:

Pred. No.:	0	Length:	8645
Score:	14495.00	Matches:	2721
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	16	Gaps:	0

US-10-038-854-38 (1-2721) x US-10-038-854-37 (1-8645)

us-10-038-854-38

GenCore version 5.1.6

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 29, 2004, 17:19:17 ; Search time 23977 Seconds
(without alignments)
5366.613 Million cell updates/sec

Title: US-10-038-854-38

Perfect score: 14495

Sequence: 1 MDVKERRPYCSLTKSRREKE.....ELADSANNIQFLRQSEIGRR 2721

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=GenEmb1 -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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us-10-038-854-38
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14495	100.0	8645	6	AX662355	AX662355 Sequence
2	14475	99.9	8675	6	AX662353	AX662353 Sequence
3	14248	98.3	8964	6	AX952856	AX952856 Sequence
4	14248	98.3	8964	10	AB025412	AB025412 Mus muscu
5	13944.5	96.2	8473	6	AX662357	AX662357 Sequence
6	13834	95.4	8487	6	AX662359	AX662359 Sequence
7	12351	85.2	7816	10	AF195418	AF195418 Mus muscu
8	11770.5	81.2	6751	6	CQ716754	CQ716754 Sequence
9	11633	80.3	8816	5	AB026979	AB026979 Danio rer
10	10403	71.8	8689	6	AX250067	AX250067 Sequence
11	10403	71.8	8689	10	AF086607	AF086607 Rattus no

12	10394.5	71.7	8409	5	GGA279031	AJ279031 Gallus ga.
13	10394.5	71.7	8409	6	AX250068	AX250068 Sequence
14	10394	71.7	8575	6	AX921803	AX921803 Sequence
15	10393.5	71.7	8797	6	CQ777485	CQ777485 Sequence
16	10393.5	71.7	8797	6	AX250063	AX250063 Sequence
17	10393.5	71.7	8797	6	AX250066	AX250066 Sequence
18	10393.5	71.7	8797	10	AB025411	AB025411 Mus muscu
19	10329.5	71.3	8438	6	AX675551	AX675551 Sequence
20	10310.5	71.1	9729	6	AX250013	AX250013 Sequence
21	10309	71.1	9826	6	AX250008	AX250008 Sequence
22	10221	70.5	8354	6	AX556500	AX556500 Sequence
23	10189	70.3	8585	10	AB025413	AB025413 Mus muscu
24	10144.5	70.0	8645	6	AX600210	AX600210 Sequence
25	10001	69.0	9722	10	AF059485	AF059485 Mus muscu
26	9764.5	67.4	9264	5	AB026980	AB026980 Danio rer
27	9489	65.5	5804	10	AK122513	AK122513 Mus muscu
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29	9267	63.9	5309	9	AB040888	AB040888 Homo sapi
30	9194	63.4	7514	6	CQ722991	CQ722991 Sequence
31	9035	62.3	8118	5	GGA238613	AJ238613 Gallus ga
32	8993.5	62.0	7713	9	BSM808325	BX648178 Homo sapi
33	8972	61.9	8373	10	AB025410	AB025410 Mus muscu
34	8884	61.3	8297	9	AF100772	AF100772 Homo sapi
35	8663	59.8	7706	6	CQ714850	CQ714850 Sequence
36	8463.5	58.4	7781	9	AB032953	AB032953 Homo sapi
37	6702.5	46.2	6560	6	AX250065	AX250065 Sequence
38	5955.5	41.1	3394	9	AK125869	AK125869 Homo sapi
39	5714	39.4	3614	6	AX876525	AX876525 Sequence
40	5714	39.4	3614	6	BD156175	BD156175 Primer fo
41	5714	39.4	3614	9	AK001336	AK001336 Homo sapi
42	5313	36.7	8993	9	BSM806812	BX640737 Homo sapi
43	5117	35.3	3270	6	AX877449	AX877449 Sequence
44	5117	35.3	3270	6	BD156663	BD156663 Primer fo
45	5117	35.3	3270	9	AK001748	AK001748 Homo sapi

Search completed: December 30, 2004, 05:27:18
Job time : 25852 secs